



# SEQUENCE LISTING

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<120> HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 MOLECULES AND  
METHODS OF TREATMENT THEREWITH

<130> 08702.0081-00000

<140> 09/249,011

<141> 1999-02-12

<160> 52

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Murine anti-B7-2 heavy chain

<220>

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<222> (1)..(405)

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48

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

gtg cac tcc cag gtc cag ctg cag cag tct ggg cct gag ctg gtg agg  
96

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg  
20 25 30

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cct ggg gaa tca gtg aag att tcc tgc aag ggt tcc ggc tac aca ttc  
144

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
35 40 45

act gat tat gct ata cag tgg gtg aag cag agt cat gca aag agt cta  
192

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac  
240

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc  
288

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
85 90 95

F4 aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc  
336

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga  
384

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

acc tca gtc acc gtc tcc tca  
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Thr Ser Val Thr Val Ser Ser  
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<213> Murine anti-B7-2 heavy chain

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Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg  
20 25 30

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
100 105 110

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Thr Ser Val Thr Val Ser Ser  
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1 5 10 15

ggt acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct  
96

Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala  
20 25 30

gtg tca gca gga gag aag gtc act atg agc tgc aaa tcc agt cag agt  
144

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag  
192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg  
240

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat  
288

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat  
336

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag  
384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
115 120 125

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<213> Murine anti-B7-2 light chain

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Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
115 120 125

Leu Glu Ile Lys  
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<213> Humanized murine anti-human B7-2 heavy chain

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48

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag  
96

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc  
144

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc  
192

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac  
240

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc  
288

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
85 90 95

aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt  
336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt  
384

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

acc ctt gtc acc gtc tcc tca  
405

Thr Leu Val Thr Val Ser Ser  
130 135

<210> 6  
<211> 135  
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<213> Humanized murine anti-human B7-2 heavy chain

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Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
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Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Leu Val Thr Val Ser Ser  
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<210> 7  
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1 5 10 15

ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct  
96

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt  
144

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag  
192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg  
240

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat  
288

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat  
336

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag  
384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
115 120 125



gtg gaa ata aaa  
396  
Val Glu Ile Lys  
130

<210> 8  
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<213> Humanized murine anti-human B7-2 light chain  
  
<400> 8

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser  
1 5 10 15

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
115 120 125

Val Glu Ile Lys  
130

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gat tat gct ata cag  
15  
Asp Tyr Ala Ile Gln  
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<210> 10  
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<220>  
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<400> 10

Asp Tyr Ala Ile Gln  
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<210> 11  
<211> 51  
<212> DNA  
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<221> CDS  
<222> (1)..(51)

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48

Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
1 5 10 15

ggc

51

Gly

<210> 12

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 of humanized murine anti-human B7-2 heavy chain

<400> 12

Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
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Gly

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> CDR3 of humanized murine anti-human B7-2 heavy chain

<221> CDS

<222> (1)..(21)

<400> 13

gcg gcc tgg tat atg gac tac  
21

Ala Ala Trp Tyr Met Asp Tyr  
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<210> 14  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> CDR3 of humanized murine anti-human B7-2 heavy chain  
  
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Ala Ala Trp Tyr Met Asp Tyr  
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<210> 15  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> CDR1 of humanized murine anti-human B7-2 light chain  
  
<221> CDS  
<222> (1)..(51)

<400> 15  
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Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
1 5 10 15

gct  
51  
Ala

<210> 16  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CDR1 of humanized murine anti-human B7-2 light chain  
  
<400> 16

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
1 5 10 15

Ala

<210> 17  
<211> 21  
<212> DNA  
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<220>  
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<221> CDS  
<222> (1)..(21)

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21  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 18  
<211> 7  
<212> PRT  
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<220>  
<223> CDR2 of humanized murine anti-human B7-2 light chain

<400> 18

Trp Ala Ser Thr Arg Glu Ser  
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<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> CDR3 of humanized murine anti-human B7-2 light chain

<221> CDS

<222> (1)..(24)

<400> 19

acg caa tct tat aat ctt tac acg

24

Thr Gln Ser Tyr Asn Leu Tyr Thr

1

5

<210> 20

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of humanized murine anti-human B7-2 light chain

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5

<210> 21

<211> 405

<212> DNA

<213> Murine sp.

<220>

<221> CDS

<222> (1)..(405)

<223> Anti-B7-2 heavy chain

<400> 21

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48

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly

1

5

10

15

gtg cac tcc cag gtc cag ctg cag cag tct ggg cct gag ctg gtg agg

96

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg

20

25

30

cct ggg gaa tca gtg aag att tcc tgc aag ggt tcc ggc tac aca ttc  
144

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
35 40 45

act gat tat gct ata cag tgg gtg aag cag agt cat gca aag agt cta  
192

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac  
240

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc  
288

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
85 90 95

aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc  
336

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga  
384

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

acc tca gtc acc gtc tcc tca  
405

Thr Ser Val Thr Val Ser Ser  
130 135

<210> 22

<211> 135

<212> PRT

<213> Murine sp.

<220>

<223> Anti-B7-2 heavy chain

<400> 22

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
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Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg  
20 25 30

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Ser Val Thr Val Ser Ser  
130 135

<210> 23  
<211> 396  
<212> DNA  
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<220>  
<221> CDS  
<222> (1)..(396)  
<223> Anti-B7-2 light chain

<400> 23  
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48  
Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser  
1 5 10 15

ggg acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct  
96



Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala  
20 25 30

gtg tca gca gga gag aag gtc act atg agc tgc aaa tcc agt cag agt  
144

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag  
192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg  
240

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat  
288

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat  
336

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag  
384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
115 120 125

ctg gaa ata aaa  
396

Leu Glu Ile Lys  
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<210> 24

<211> 132

<212> PRT

<213> Murine sp.

<220>

<223> Anti-B7-2 light chain

<400> 24

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1 5 10 15

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20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
115 120 125

Leu Glu Ile Lys  
130

<210> 25

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(405)

<400> 25

atg ggt tgg aac tgt atc atc ttc ttt ctg gtt acc aca gct aca ggt  
48

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag  
96

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc  
144

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc  
192

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac  
240

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc  
288

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
85 90 95

aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt  
336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt  
384

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

acc ctt gtc acc gtc tcc tca  
405

Thr Leu Val Thr Val Ser Ser  
130 135

<210> 26

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 heavy chain

<400> 26

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
115 120 125

Thr Leu Val Thr Val Ser Ser  
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<210> 27

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<212> DNA

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<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(396)

<400> 27

atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta tgg gta tct  
48

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser  
1 5 10 15

ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct  
96

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt  
144

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag  
192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg  
240

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat  
288

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat  
336

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag  
384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
115 120 125

gtg gaa ata aaa  
396

Val Glu Ile Lys  
130

<211> 132  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 light chain

<400> 28

Met	Asp	Ser	Gln	Ala	Gln	Val	Leu	Ile	Leu	Leu	Leu	Trp	Val	Ser	
1				5					10				15		
Gly	Thr	Cys	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala
			20					25					30		
Val	Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser
		35					40					45			
Leu	Leu	Asn	Ser	Arg	Thr	Arg	Glu	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln
	50					55					60				
Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg
65					70					75					80
Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
				85					90					95	
Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr
			100					105					110		
Tyr	Cys	Thr	Gln	Ser	Tyr	Asn	Leu	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		115					120					125			
Val	Glu	Ile	Lys												
		130													

<210> 29  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR1 of  
humanized murine anti-human B7-2 heavy chain

<220>

<221> CDS  
<222> (1)..(15)

<400> 29  
gat tat gct ata cag  
15  
Asp Tyr Ala Ile Gln  
1 5

<210> 30  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR1 of humanized  
murine anti-human B7-2 heavy chain

<400> 30  
Asp Tyr Ala Ile Gln  
1 5

<210> 31  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR2 of  
humanized murine anti-human B7-2 heavy chain

<220>  
<221> CDS  
<222> (1)..(51)

<400> 31  
gtt att aat att tac tat gat aat aca aac tac aac cag aag ttt aag  
48  
Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
1 5 10 15

ggc  
51  
Gly

<210> 32  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR2 of humanized  
murine anti-human B7-2 heavy chain

<400> 32

Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys
1				5				10					15		

Gly

<210> 33  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of  
humanized murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(21)

<400> 33

gcg	gcc	tgg	tat	atg	gac	tac
21						
Ala	Ala	Trp	Tyr	Met	Asp	Tyr
1				5		

<210> 34  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of humanized  
murine anti-human B7-2 heavy chain

<400> 34



Ala Ala Trp Tyr Met Asp Tyr  
1 5

<210> 35

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR1 of  
humanized murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(51)

<400> 35

aaa tcc agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg  
48

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
1 5 10 15

gct

51

Ala

<210> 36

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR1 of humanized  
murine anti-human B7-2 light chain

<400> 36

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
1 5 10 15

Ala

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR2 of  
humanized murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(21)

<400> 37

tgg gca tcc act agg gaa tct

21

Trp Ala Ser Thr Arg Glu Ser

1

5

<210> 38

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR2 of humanized  
murine anti-human B7-2 light chain

<400> 38

Trp Ala Ser Thr Arg Glu Ser

1

5

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of  
humanized murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(24)

<400> 39

acg caa tct tat aat ctt tac acg

24

Thr Gln Ser Tyr Asn Leu Tyr Thr  
1 5

<210> 40

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of humanized  
murine anti-human B7-2 light chain

<400> 40

Thr Gln Ser Tyr Asn Leu Tyr Thr  
1 5

<210> 41

<211> 1960

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (12)..(408)

<220>

<221> CDS

<222> (768)..(1087)

<400> 41

tctagaccac c atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta  
50

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu  
1 5 10

tgg gta tct ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat  
98

Trp Val Ser Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp  
15 20 25

tcc ctg gct gta agc tta gga gag agg gcc act att agc tgc aaa tcc  
146

Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser  
30 35 40 45

agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg  
194

Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp  
50 55 60

tac cag cag aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca  
242

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala  
65 70 75

tcc act agg gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct  
290

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser  
80 85 90

ggg aca gat ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg  
338

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val  
95 100 105

gca gtt tat tac tgc agc caa tct tat aat ctt tac acg ttc gga cag  
386

Ala Val Tyr Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln  
110 115 120 125

ggg acc aag gtg gaa ata aaa c gtaagtagtc ttctcaactc tagaaattct  
438

Gly Thr Lys Val Glu Ile Lys  
130

aaactctgag ggggtcggat gacgtggcca ttctttgcct aaagcattga gtttactgca  
498

aggtcagaaa agcatgcaaa gccctcagaa tggtcgcaaa gagctccaac aaaacaattt  
558

agaactttat taaggaatag ggggaagcta ggaagaaact caaaacatca agattttaaa  
618

tacgcttctt ggtctccttg ctataattat ctgggataag catgctgttt tctgtctgtc  
678

cctaacatgc cctgtgatta tccgcaaaca acacacccaa gggcagaact ttgttactta  
738

aacaccatcc tgtttgcttc tttcctcag ga act gtg gct gca cca tct gtc  
790

Arg Thr Val Ala Ala Pro Ser Val  
135 140

ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct  
838

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser  
145 150 155

gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag  
886

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln  
160 165 170

tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc  
934

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val  
175 180 185

aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg  
982

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu  
190 195 200

acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa  
1030

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu  
205 210 215 220

gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg  
1078

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg  
225 230 235

gga gag tgt tagagggaga agtgccccca cctgctcctc agttccagcc  
1127

Gly Glu Cys

tgacccctc ccattctttg gcctctgacc ctttttccac aggggaccta ccctattgc  
1187

ggctctccag ctcatctttc acctcaccce cctcctcctc cttggcttta attatgctaa  
1247

tgttggagga gaatgaataa ataaagtga tctttgcacc tgtgggtttct ctctttcctc  
1307

atttaataat tattatctgt tgttttacca actactcaat ttctcttata agggactaaa  
1367

tatgtagtca tcctaaggcg cataaccatt tataaaaatc atccttcatt ctattttacc  
1427

ctatcatcct ctgcaagaca gtccctccctc aaaccacaaa gccttctgtc ctcacagtcc  
1487

cctggggccat ggtaggagag acttgcttcc ttgttttccc ctcttcagca agccctcata  
1547

gtccttttta agggtgacag gtcttacagt catatatcct ttgattcaat tccctgggaa  
1607

tcaaccaaag caaatttttc aaaagaagaa acctgctata aagagaatca ttcattgcaa  
1667

catgatataa aataacaaca caataaaagc aattaaataa acaaacaata gggaaatggt  
1727

taagttcatc atgggtactta gacttaatgg aatgtcatgc cttatttaca tttttaaaca  
1787

ggtactgagg gactcctgtc tgccaagggc cgtattgagt actttccaca acctaattha  
1847

atccacacta tactgtgaga ttaaaaacat tcattaaaat gttgcaaagg ttctataaag  
1907

ctgagagaca aatatattct ataactcagc aatcccactt ctaggatcaa ttc  
1960

<210> 42

<211> 239

<212> PRT

<213> Mus sp.

<400> 42

Met	Asp	Ser	Gln	Ala	Gln	Val	Leu	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser
1				5					10					15	

Gly	Thr	Cys	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala
			20					25						30	



<221> CDS

<222> (12)..(417)

<220>

<221> CDS

<222> (655)..(948)

<220>

<221> CDS

<222> (1341)..(1376)

<220>

<221> CDS

<222> (1495)..(1821)

<220>

<221> CDS

<222> (1919)..(2238)

<400> 43

tctagaccac c atg ggt tgg aac tgt atc atc ttc ttt ctg gtt acc aca  
50

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr  
1 5 10

gct aca ggt gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag  
98

Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu  
15 20 25

gtg aag aag cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc  
146

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly  
30 35 40 45

tac aca ttc act gat tat gct ata cag tgg gtg aga cag gct cct gga  
194

Tyr Thr Phe Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly  
50 55 60

cag ggc ctc gag tgg att gga gtt att aat att tac tat gat aat aca  
242

Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr  
65 70 75

aac tac aac cag aag ttt aag ggc aag gcc aca atg act gta gac aag  
290



Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys  
80 85 90

tcg acg agc aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat  
338

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp  
95 100 105

acg gcc gtt tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg  
386

Thr Ala Val Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp  
110 115 120 125

ggt caa ggt acc ctt gtc acc gtc tcc tca g gtgagtcctt aaaacctcta  
437

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
130 135

gagctttctg gggcgagccg ggcctgactt tggctttggg gcagggagtg ggctaagggtg  
497

aggcaggtgg cgccagccag gtgcacaccc aatgcccgtg agcccagaca ctggaccctg  
557

cctggaccct cgtggataga caagaaccga ggggcctctg cgccctgggc ccagctctgt  
617

cccacaccgc ggtcacatgg caccacctct cttgcag cc tcc acc aag ggc cca  
671

Ala Ser Thr Lys Gly Pro  
140

tcg gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca  
719

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
145 150 155

gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg  
767

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
160 165 170

gtg tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca  
815

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
175 180 185

gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc  
863

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
190 195 200 205

gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat  
911

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
210 215 220

cac aag ccc agc aac acc aag gtg gac aag aca gtt g gtgagaggcc  
958

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val  
225 230

agctcagggg gggaggggtgt ctgctggaag ccaggctcag ccctcctgcc tggacgcacc  
1018

ccggctgtgc agccccagcc cagggcagca aggcaggccc catctgtctc ctcacccgga  
1078

ggcctctgcc cgccccactc atgctcaggg agaggggtctt ctggcttttt ccaccaggct  
1138

ccaggcaggc acaggctggg tgccccctacc ccaggccctt cacacacagg ggcagggtgct  
1198

tggctcagac ctgccaaaag ccatatccgg gaggaccctg ccctgacct aagccgaccc  
1258

caaaggccaa actgtccact ccctcagctc ggacaccttc tctcctccca gatccgagta  
1318

actcccaatc ttctctctgc ag ag cgc aaa tgt tgt gtc gag tgc cca ccg  
1369

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro  
235 240

tgc cca g gtaagccagc ccaggcctcg ccctccagct caaggcgga caggtgccct  
1426

Cys Pro  
245

agagtagcct gcatccaggg acaggcccca gctgggtgct gacacgtcca cctccatctc  
1486

ttcctcag ca cca cct gcg gca gca ccg tca gtc ttc ctc ttc ccc cca  
1535

Ala Pro Pro Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro  
250 255

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc  
1583

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
260 265 270 275

gtg gtg gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg  
1631

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp  
280 285 290

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag  
1679

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
295 300 305

gag cag ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg  
1727

Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val  
310 315 320

cac cag gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac  
1775

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
325 330 335

aaa ggc ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa g  
1821

Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys  
340 345 350

gtgggacccg cggggatatga gggccacatg gacagaggcc ggctcggccc accctctgcc  
1881

ctgggagtga ccgctgtgcc aacctctgtc cctacag gg cag ccc cga gaa cca  
1935

Gly Gln Pro Arg Glu Pro  
355 360

cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag  
1983

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
365 370 375

gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc  
2031

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
380 385 390

gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc aca  
2079

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
395 400 405

cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc  
2127

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
410 415 420

acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc  
2175

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
425 430 435 440

gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc  
2223

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
445 450 455

ctg tcc ccg ggt aaa tgagtgaatt c  
2249

Leu Ser Pro Gly Lys  
460

<210> 44

<211> 461

<212> PRT

<213> Mus sp.

<400> 44

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	50	55	60
Glu	Trp	Ile	Gly	Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	Asn	Tyr	Asn	65	70	75
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Lys	Ser	Thr	Ser	85	90	95
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	100	105	110
Tyr	Tyr	Cys	Ala	Arg	Ala	Ala	Trp	Tyr	Met	Asp	Tyr	Trp	Gly	Gln	Gly	115	120	125
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	130	135	140
Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	145	150	155
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	165	170	175
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	180	185	190
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	195	200	205
Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	210	215	220
Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	225	230	235
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Ala	Ala	Ala	Pro	Ser	Val	Phe	Leu	245	250	255
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	260	265	270
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	275	280	285
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	290	295	300

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu  
305 310 315 320

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys  
325 330 335

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys  
340 345 350

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser  
355 360 365

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys  
370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln  
385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly  
405 410 415

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln  
420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn  
435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
450 455 460

<210> 45

<211> 327

<212> DNA

<213> Homo sapiens

<400> 45

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc  
60

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca  
120

gggaaagttc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct  
180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct  
240

gaagatgttg caacttatta ctgtcaaaag tataacagtg cccctccgag tacgttcggc  
300

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327

<210> 46  
<211> 339  
<212> DNA  
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<400> 46  
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120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctaccggg  
180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc  
240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact  
300

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339

<210> 47  
<211> 95  
<212> PRT  
<213> Homo sapiens

<400> 47

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile  
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro  
85 90 95

<210> 48  
<211> 101  
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<400> 48

Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly  
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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Asn Lys Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro  
35 40 45

Pro Lys Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80



Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro  
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<211> 368  
<212> DNA  
<213> Homo sapiens

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120

ctggacaagg gcttgagtgg atgggaagga tcatgcctat ccttggacta gcaaattacg  
180

cacagaagtt ccagggcaga gtcacgatta ccgcggacaa atccacgagc acagcctaca  
240

tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg agagatcccg  
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attatgtttg ggggagcgac aactggttcg acccctgggg ccaggggaacc ctgctcatcg  
360

tctcctca  
368

<210> 50  
<211> 358  
<212> DNA  
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<400> 50  
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120

ggaaggggct ggagtgggtg gttaatataa tggtagtcgg aattgaacca tactatgcgg  
180

actctgtgaa gggccgattc accatctcca gaggcaacgc caagaactca ctgtatctgc  
240

aatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcgaga gggatctgtc  
300

ttatgacaga ggctactttg actactgggg ccagggaacc ctggtcacgc tctctca  
358

<210> 51

<211> 97

<212> PRT

<213> Homo sapiens

<400> 51

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser  
1 5 10 15

Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Thr  
20 25 30

Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
35 40 45

Arg Ile Met Pro Ile Leu Gly Leu Ala Asn Tyr Ala Gln Lys Phe Gln  
50 55 60

Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met  
65 70 75 80

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg

<210> 52  
<211> 98  
<212> PRT  
<213> Homo sapiens

<400> 52

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser  
1 5 10 15

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr  
20 25 30

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
35 40 45

Tyr Ile Ser Ser Arg Gly Ser Glu Thr Ile Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg